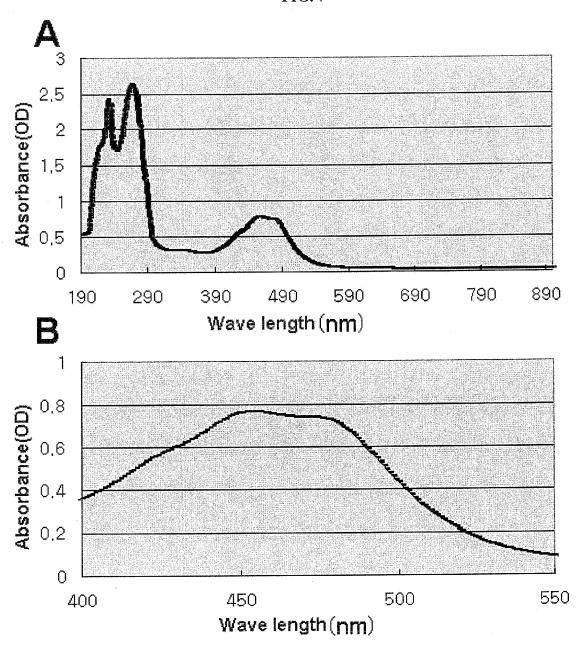


IG. 6

FIG. 7



IIG. 8

99 LYAGES WPKLIAKHMI HBRHAGID ND PD FGBG---GPVRWYGSFVS TYPGWRBGLLLP VI YTTYALILGD-RWWYYLP WP VP AVLASIOI FYFGIWLD HR GPYBNYASFI TYFGWREGLLLPYIYTVYALILGD BWNYVIFWPLPAILASIQLFVFGTWLPHR (1) MHAATAKATEFGASTRDDARQRBVGLTLAAVIIAAMLVEBVGLMFFWPLTLHSLLPALPLVVLQTWLYVGLFIIAHDCMHGSLYFFKPQVWRRIGQLCLF T V L LSAAIIAAWLYLBY LWFLDAAAHPLLAIL LLGIT WLSVGLFIIAHDAMHGSVYPGRPRANAAIGOL LW (90) LYAGES WAKANIVARNAHHRHIGIDDDPDFDFDHG---GPVRWYARFIGIYFGWREGILLPVIYTVYALILGD-BWNYWYEWPLPSILASIQLFVFGTWLPHR (101) LYAGESEDALNVEHRKHERHPGTAEDPDEDEVPPHGFWINVFASFFILHYFGWKQYALIAAYSLYYQLYFAYPLQNILLFWALPGLISALQLFTFGTYLDHK INS AHALDKADLI ATSLITYSGGI IAANLALHVHALUFILDAAAHDI LAIANFIGII-ULS YGLFFI AUDANHGS VYPGDDPKGNAANGQIYUU INS GERIPGITODITANI GLI AAT LLCOLVLHAFTL WILDAAAHDILAVI.CLAGIT-WIS VGLFIT AHDANHOSS VVPGRPRANAALGOLALW 땑 PATOPFADRHNARTSEFPAULSLITCFHFG-FRHEHHLHPDAPWWRLPELKKRALEBRD PGED AEPDRHNARSKEISDPYSLLICFHFGGYHHEHELEPTYPWWRLPSIRIKGDIA--PGHDDFPDRHNARSTGIGDPLSLLICEBFGGFIHEHHLHPHWRLPRIRIGGBA-PGHD FPDRHMARSS I DPLSLLTCFHFGGYRHEHHLHP YPWWRLP TRKKG (101) LYAGESW KLIVKHM HHRH GTDDDPDFDHG る (201)(301)(E) 88 \equiv 8 \Box P. haeundaesis Bradyrhizobium_sp Consensus Bradyrhizobium_sp P. haeundaesis රගානමාන Alcaligenes_sp Alcaligenes_sp P. haeumdaesis Alcaligenes_sp Bradyrhizobium_sp Consensus

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P. baeundaesis (1) binfilyvalulvabilaksyhkulnhgplomovhkshhebbbhlekndlyglyfalafylffognlvarylomlalchlyfolhpolyhgr

Alcaligenes_sp (1) NTQFLITVATYLYNELTATSYBRWINHSPLGWGWHKSHHEEDDHALERNDLYGRYFAYLATILFTYGAYWWPYDWDALGMTYYGLIYFILHDGLYHQRW

(1) MINELLYVATYLYBELTAYSVHRWINHGPLGWGWHKSHHEEHDHALEKNDLYGLYFAYLATILETYG W PYLWWIALGWYYGLIYFILHDGLYBQRW Consensus

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P. haeundaesis (101) PFRYIPRKGYARRIYQAHRIHHAVBGRDHCYSFGFIYAPPYDKIKQDIKTSGYLRABAQERT Alcaligenes_sp (101) PFRYIPRRYFRRIYQAHRIHHAVBGRDBCYSFGFIYAPPYDKIKQDIKRSGYLRPQDBRPS

Consensus (101) PERVIPRAGY RRIYQAHRIHHAVBGRDHCVSFGFIYAPPVDKLKQDLK SGVLR

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P. haeundaesis Flavobacterium_sp Consensus	8 8 8	1 (1) VTHDVLLAGAGLANGLIALALBAARPDLRVLLDHAAGPSIGHFWSCHDPDLSPHWLARLKPLRBANWPDQEVRFPRHABRLAFGYGSLDGAALADAVAR (1) NSHDLLIAGAGLSGALIALAVBDRRPDAŘIVMLDARSGESDQHFWSCHDFDLSPEWLARLSPIRBGEWTDQEVAFPDHSBRLTFGYGSIBAGLIGLLQ- (1) NSHDLLIAGAGLA ALIALALR RPD RILLLD AGPSD HFWSCHD DLSP WLARL PIRRA W DQEV FP HARRL TGYGSIDAAAL L
P. haeundaesis Flavobacterium_sp Consensus	(101)	101 (101) SCAEIBWNSDIALLDEQGATLSCGTRIEAGAYLDGRGAQPSRHLTYGEQKFYGYELETDCPHGYPRPMINDATYTQQDGYRFIYLLFFSPTRILIEDTRY (100) -GYDLRWNTBYATLDDTGATLTDGSRIEAACYIDARGAYETPHLTYGFQKFYGYELETDAPHGYERPWINDATYPQNDGYRFIYLLPFSPTRILIEDTRY (101) G DIRWNS IA LDD GATLS GSRIEAA YIDARGA S HLTYGFQKFYGYEIETD PHGY RPWINDATY Q DGYRFIYLLPFSPTRILIEDTRY
P. haeundaesis Elavobacterium_sp Consensus	(201) (199) (201)	201 SDGGNLDDDALAASEDPARQQGWTGAEVBEERGILPTALAHDAAGFWADHAEGPPPVGLRAGFFHPVTGYSLPYAAQVADVVAGLSGPPGTDALEGAIR (199) SDGGDLDDGALAQASLDFAARRGWTGQENBEERGILPTALAHDAIGFWRDHAQGAVPVGLGAGLFHPVTGYSLPYAAQVADALAAR-DLTTASARRAVB (201) SDGG LDD ALA AS DYA GWTG ENBRERGILPTALAHDA GFW DHA G VPVGL AG FHPVTGYSLPYAAQVAD IAA T A R AIR
P. haeundaesis Flavobacterium.sp Consensus	(301)	301 (301) DYAIDBARRDRFLREINRMERGCAPDRRYTLIQRFYRHPHGLIERFYAGBLSVADQLRIVTGRPPIBLGTAIRCLPERPILKENA (237) GWAIDRADDRDRFLRILNRMERGCPPDRRYLLIQRFYRLPRPFRAGRLTLADRENIVTGRPPIPLSQAVRCLPERPLLIGERA (301) WAIDRA KDRFLRILNRMERGC PDRRY LLQRFYRLP LIERFYAGRLSLAD LRIVTGRPPIPL AIRCLPERPLL E A

FIC 12

101 (101) GKVFDVVNBADQLERQIAQFND DDLEGYRRFRDVAEEVVQEGYVKLGTVPFLKLGQMLKAAPALMKLEAVKSVHAKVATFIKDPYLRQAFSYHTLLVGGN (94) GRSFEFVNDDDELLRQVASFNPADVDGYRRFHDVAEEVVREGYLKLGTTPFLKLGOMLNAAPALMKLQAYRSVHSNVARFIQDPHLRQAFSFHTLLVGGN (101) GK FDVVND D.L. RQIA FNP DLDGYRRF DVAEEVY EGYLKLGT PFLKLGOML AAPALMKL AYKSVHA VA FI DPHLRQAFSFHTLLVGGN	201) PESTSSIYALIHALERRGGVWFAKGGTNQLVAGBVALFERLGGQMMLNAKVARIETEGARTIGVTLADGRSLRADBVASNGDVWHNYRDLIGHTARGQSR (194) PESTSSIYALIHALERRGGVWFAKGGTNQLVAGBVALFERLGGTLLLNARVTRIDTEGDRATGVTLLDGRQLRADTVASNGDVWHSYRDLLGHTRKGRTK (201) PESTSSIYALIHALERRGGVWFAKGGTNQLVAGBVALFERLGG LLLNAKV RIDTEG R TGVTL DGR LRAD VASNGDVWH YRDLIGHT RG SK	301 (301) AKSLDRKRWS MSLFVLHEGLREARKDIAHHTILFGPRYRELVNEIFKGPKLAEDFSLYLHSPCTTDPDMAPPGMSTHYVLAPVPHLGRAEIDWAVEGPRY (294) AAILNBQRWS MSLFVLHFGLSKRPENLAHHSVIFGPRYKGLVNEIFNGPRLPDDFS MYLHSPCYTDPSLAPEGMSTHYVLAPVPHLGRADVDWEAEAPGY (301) A L R RWSMSLFVLHFGL P IAHHSIIFGPRYK LYNEIF GPKL DDFSLYLHSPC TDP LAP GMSTHYVLAPVPHLGRADIDW EAP Y	401 (401) ADRILASLEBERITPNLEANLTITRIPTPADFASELNABHGSAES VEPILIOS AWFRPHNEDKTIRNPYLYGAGT HPGAGIPGYVGS AKATAQVNLSDLAG (S94) AERIFEELERRAIPDLRKHLIVSRIFSPADFSTELS AHHGSAES VEPILIOS AWFRPHNEDK I NFYIYGAGT HPGAGIPGYVGS AKATAQVNLSDLAV (401) ADRI LE R IP LR LI SRIFSPADFASEL AHHGSAES VEPILIOS AWFRPHNEDK I NFYIYGAGTHPGAGIPGYVGS AKATAQVNLSDLA 501	(501) A
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P. haeundaesi: Flavobacterium_sy Consensus	P. haeundaesi: Flavobacterium_sn Consensux	P. haeundaesi: Flavobacterium_s	P. haeundaesi Flavobacterium_s Consensu	P. haeumdaesis
	200 P. baeundaesis (101) GKVFDYVNEADQLERQIAQFNPDDLEGYRRFRDYAEEVYQEGYVKLGTVPFLKLGQMLKAAPALMKLEAYKSVHAKVATEIKDPYLBQAFSYHTLLVGGN Flavobacterium_sp (94) GRSFEYVNDDDELLBQYASFNPADYDGYRRFHDYAEEVYREGYLKLGTTPFLKLGQMLNAAPALMKLGAYRSVHSNYARFIQDPHLRQAFSFHTLLVGGN Consensus (101) GK FDYVND D L RQIA FNP DLDGYRRF DYAEEVY EGYLKLGT PFLKLGQML AAPALMKL AYKSVHA YA FI DPHLRQAFSFHTLLVGGN	-	101 (101) GRVEDVYNEADQLEBGLAQFRPDDLEGYRRFBDYAEEVYDEGYVKLGTVPFLKLGOMLKAAPALMKLEAYKSVHAKVATFIKDPYLRQAFSTHTL (94) GRSFEYNDDDELIBGYASFNPADVDGTRRFHDYAEEVYBEGYLKLGTTPFLKLGOMLNAAPALMKLEAYKSVHAKVATFIKDPYLRQAFSTHTL (101) GK FDYYND D L RQIA FNP DLDGYRRF DYAEEVY EGYLKLGT PFLKLGOML AAPALMKL AYKSVHA VA FI DPHLRQAFSFHTL (201) GR FDYYND D L RQIA FNP DLDGYRRF DYAEEVY EGYLKLGT PFLKLGOML AAPALMKL AYKSVHA VA FI DPHLRQAFSFHTL (201) PFSTSSIYALIHALERBGGVWFAKGGTNQLVAGNVALFERLGGTLLLNARVRRIFFEGARTIGVTLADGRGLRADVASNGDVHNVRDLIGHTR (201) PFSTSSIYALIHALERBGGVWFAKGGTNQLVAGNVALFERLGGTLLNARVR RIDTEG R TGVTL DGR LRAD VASNGDVMH YRDLLGHTR (201) RKSLDRKRWSMSLFVLHFGLREAPKDIAHHTLFGPRYRELVNEFRGPKLAEDFSLYLHSPCTTDEDMAFPGBSTHYLAPVPHLGRAELDWAV (204) AKSLDRKRWSMSLFVLHFGLREAPKDIAHHTLFGPRYRELVNEFRGPKLAEDFSLYLHSPCTTDEDMAFPGBSTHYLAPVPHLGRAELDWAV (204) AKILNBCRWSMSLFVLHFGLREAPKDIAHHTLFGPRYRELVNEFRGPKLAEDFSLYLHSPCTTDEDMAFPGBSTHYLAPVPHLGRAEDDWAV (204) AAILNBCRWSMSLFVLHFGL P IAHHSIIFGPRYR LYNEIF GPKL DDFSLYLHSPCTTDEDMAFPGBSTHYVLAPVPHLGRADDWAV (301) A L R RWSWSLFYLHFGL P IAHHSIIFGPRYR LYNEIF GPKL DDFSLYLHSPC TDP LAP GMSTHYVLAPVPHLGRADDWAV (301) A L R RWSWSLFYLHFGL	101 (101) GRYPDYWAEADQLERGIAGFNEDDLEGYRREBDYAEETYGGGTVKLGTYPELKLGOMLKAAR ALMKLEAYKS YHAKVATFIKDPYLEGAFSTHTI (101) GRYPDYWEADQLERGIAGFNEDDLEGYRREHDYAEETYGGGTVKLGTTPFLKLGOMLNAAR ALMKLAYRS YHSWYARFIQDPHLRGAFSHTI (201) GR FDYVND D.L BOLA FNP DLDGYRRE DYAEEYYBGGTKLGT FFLKLGOML AAPALMKL AYKS YHSWYARFIQDPHLRGAFSHTI (201) PESTSSIYALIHALERSGGYWFAKGGTNOL YAGBYALFERLGGOLMLWARVARIHTGBARTGYTLLDGRACLEADWASNGDYHNYRDLIGHTR (201) PESTSSIYALIHALERSGGYWFAKGGTNOL YAGBYALFERLGGTLLLNARY RIDTEG R TGYTL DGR LRAD YASNGDYHNYRDLLGHTR (201) AKSLDRKEWSMSHEYHAGGRAPALHAGSTROL YAGBYALFERLGGTLLNARY RIDTEG R TGYTL DGR LRAD YASNGDYHNYRDLLGHTR (204) AKILDAERSGYWFAKGGTNOL YAGBYALFERLGGTLLNARY RIDTEG R TGYTL DGR LRAD YASNGDYHNYRDLLGHTR (204) AKILDAERSWSMSHEYLHFGLREAPKDIAHFTLFGPRYRELYNGFRLAEDFSLYLHSPCTTDFDWARPGWSTRYTHAPYRGAFRADDWA (204) AKILDAELERBLEPHLRANLTTRIFTPAPFASELWAHHGSAFSVEPILTGSAWFREPRINGNTIRNFLYNGAGTHPGAGIPGYVGSARATAQYN (304) AENIFEELERBAIPDLRYBETSPADFASELWAHHGSAFSVEPILTGSAWFREPRINGDRALWYTTRYGAGTHPGAGIPGYVGSARATAQYN (305) AENIFEELERBAIPDLRYBETSPADFASELWAHHGSAFSVEPILTGSAWFREPRINGDRALWYTTRYGAGTHPGAGIPGYVGSARATAQYN (401) ADRI LE R IP LIR LT SRIFSPADFASELAAHHGSAFSVEPILTGSAWFREPRINGDRALWYTTRYGAGTHPGAGIPGYVGSARATAQYN (401) ADRI LE R IP LIR LT SRIFSPADFASELAAHHGSAFSVEPILTGSAWFREPRINGDRALWYTTRYGAGTHPGAGIPGYVGSARATAQYN (504)

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P, haeundaesis Flavobacterium_sp Consensus	(1) NSDLVLISTBAITQGSQSFATAAKLNEPGIRDDTVNLVANCEHADDVIDGQALGSRPEAVNDEQAEDGGERVDTLAALQGDGPYTEPFAALBAVARRHDF (1) NTDLIATSBAATAGGSGSFAQAAKLNEPGIBEDTVNLYANCRHADDVILGQVNGSAFEAGGDPQARLGALBADTLAALHEDGPNSPFAALBQVARRHDF (1) NSDL IS AI QGSGSFA AAKLNEPGIRDDTVNLYANCRHADDVIDGQ LGS PEA DPQARL ALR DILAAL DGPNSPFAALR VARREDF
P. haeundaesis Flavobacterium_sp Consensus	101 (101) PQAWPNDLIEGFANDYEARDYRTLDDYLEYSYHYAGIYGYMARVUGYRDDPYLDRACDLGLAFQLINIARDYIDDARIGRCYLPGDWLDQAGARIDGPY (101) PDLWPWDLIEGFANDYADREYRSLDDYLEYSYHYAGYYGYMNARVUGYQDDAYLDRACDLGLAFQLINIARDYIDDARIGRCYLPADWLAEAGAIYBGBY (101) P WPWDLIEGFANDY RDYRSLDDYLEYSYHYAGIYGYMNARYUGY DD YLDRACDLGLAFQLINIARDYIDDA IGRCYLPADWL AGA IDGPY
P. haeundaesis Flavobacterium_sp Consensus	201 (201) PSPELYTVILRLIDEAEPYYAS ARVGLADLPPRCAWSTAAALRIYRAIGLRIBKSGPQAYRQKISTSKAAKIGLIGVGGWDYARSRLPGAGYSRQGLWTR (201) PSDALYSVIIRLIDAAEPYYAS ARQGIPHLPPRCAWSTAAALRIYRAIGTRIRQGSPEAFRQRISTSKAAKIGLLARGGLDAAASKLBGGEISBDGLWTR (201) PS LYSVIIRLID AEPYYAS AR GL LPPRCAWSTAAALRIYRAIG RIR GP AYRQRISTSKAAKIGLLA GG D A SRL GA ISR GLWTB
P. haeundaesis Flavobacterium_sp	301 (301) PHP (301) PRA-

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(1) WARDYNDIHATILQIALEELAQGAGAVSQPLGAAMSHGALSSGARFÄGNLMILAAEASGGYCDIIYDAACAVEBVHAASIIFDULPCNDDAQIARGAPAT P. haeundaesis (1) WIPROCEPLEDIVELELAQI SGOPGITIS ADIGAANS DAALSPOREËRA YLMINPAËSS OSTOCIABITIAACAVEN VHAASLI EDDINCOLDIABTRISOPAT Flavobacterium_sp

EG YS PIGAANS AALS GERREAALAIL AEASGOVCD IVDAACAVEBUHASLIFDDLPCHDDA ENG PAF r=± Ħ 日 == \equiv Consensus Ξ

P. haeundaesis (101) BYAHGESBAYLGGIALITEANALLAGARGASGIYBAQLYRILSASLGBQGICAGQDLDLHAARNGAGVEGEQDLATGYLGIENLAYIKEFDAEEQTQ

Flambacterium_sp (101) Hyabderballagiallteannicdeadgaippabarlyasusbangeycichcollardaaaterboolatgolatgolenslindidlaeted

BA LY ISRALGE GICHGODIDIBA K ANGIE BODINIGNIFIAGIENIAIIK Consensus (101) HYANGE RAYLAGIALITEAN ILA ARGAS 33 P. baeundaesis (201) MIDFGROLGEVFGSTDDLIDVVGDQAALGKDIGRDAAAPGFRRGILAVSDLQNYSBHYEASEAQLDAMLRSTRLQAPEIAALIERVLPYAABA--Ę.

(201) LINTEGROEGRYFGS YDDELDYT GDRAST GROF ARDT ARPGPROGLINAVOQUODY AQHYBASBAQLD ELIKTBLFROOQLADLLARVLP HDIBBSA Flavobacterium_sp

A IA LL BYLPH (201) LI FORQIORYFOSYDDILDYIOD AA GKDIARD AAPODK GILAY L YA HY ASBAQLD LIRSK Consensus



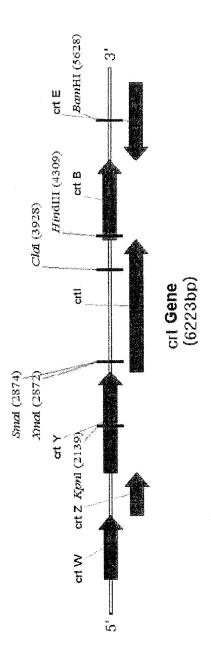


FIG. 16

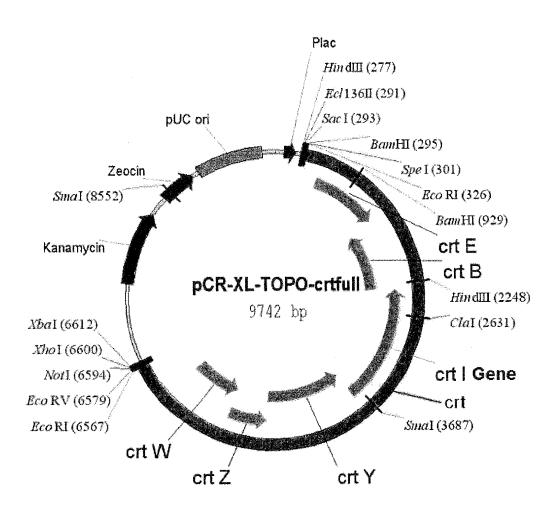


FIG. 17

